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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: January 13, 2006, 09:27:05 ; Search time 27 Seconds

1 MADKGNTYSPFDVNDTLLVVR.....DMTPBTFDDDEEEEDIDI 616

Title: US-10-734-782-4
Perfect score: 3097

Sequence: 1 MADKGNTYSPFDVNDTLLVVR.....DMTPBTFDDDEEEEDIDI 616

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 826755679 residues

Total number of hits satisfying chosen parameters:

572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_A1:
 1: /cgm2_6/_ptodata/1/1aa/5_COMB_pep_*
 2: /cgm2_6/_ptodata/1/1aa/6_COMB_pep_*
 3: /cgm2_6/_ptodata/1/1aa/H_COMB_pep_*
 4: /cgm2_6/_ptodata/1/1aa/PCTUS_COMB_pep_*
 5: /cgm2_6/_ptodata/1/1aa/RB_COMB_pep_*
 6: /cgm2_6/_ptodata/1/1aa/backfiles1_pep_*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	3097	100.0	616	2	US-10-049-086-4
2	3015	97.4	616	2	US-09-690-85A-2
3	128	4.1	1095	2	US-09-206-942-45
4	128	4.1	1101	2	US-09-206-942-43
5	118	3.8	564	2	US-09-107-512A-5970
6	116.5	3.8	2042	2	US-10-192-584-6
7	116.5	3.8	2042	2	US-09-206-550B-7
8	116	3.7	1166	1	US-08-477-511-11
9	116	3.7	1781	1	US-08-477-511-11
10	115	3.7	1095	2	US-09-206-942-69
11	115	3.7	1095	2	US-10-193-764-65
12	115	3.7	1536	1	US-08-038-682-2
13	115	3.7	1536	1	US-08-302-812-2
14	115	3.7	1536	1	US-08-530-198-2
15	115	3.7	1536	1	US-08-169-880-2
16	115	3.7	1536	1	US-08-728-410-2
17	115	3.7	1536	1	US-08-617-687-2
18	115	3.7	1536	2	US-08-719-611-2
19	115	3.7	1536	2	US-09-106-942-67
20	115	3.7	1536	2	US-10-193-744-63
21	114	3.7	2048	2	US-09-268-347-48
22	114	3.7	3241	2	US-09-341-716-1
23	113	3.6	504	2	US-09-949-016-7915
24	112.5	3.6	1572	2	US-09-710-219-2906
25	112.5	3.6	4536	2	US-09-180-422B-27
26	112.5	3.6	4536	2	US-09-030-030-01
27	112.5	3.6	4563	2	US-09-108-006C-1

ALIGNMENTS

RESULT 1	US-10-049-086-4	;	;	;	;
	;	Sequence 4 , Application US/10049086	;	;	;
		Patent No. 6919083	;	;	;
		GENERAL INFORMATION:	;	;	;
		APPLICANT: Aqua Health (Europe) Limited	;	;	;
		APPLICANT: Griffiths, Steven	;	;	;
		APPLICANT: Ritchie, Rachael	;	;	;
		TITLE OF INVENTION: Sequence	;	;	;
		FILE REFERENCE: P24468-GST/RMC	;	;	;
		CURRENT APPLICATION NUMBER: US/10/049 , 086	;	;	;
		CURRENT FILING DATE: 2002-02-06	;	;	;
		PRIOR APPLICATION NUMBER: GB9318588 . 6	;	;	;
		PRIOR FILING DATE: 1999-07-08	;	;	;
		PRIOR APPLICATION NUMBER: GB0005848 . 7	;	;	;
		PRIOR FILING DATE: 2000-03-11	;	;	;
		PRIOR APPLICATION NUMBER: GB00066674 . 6	;	;	;
		PRIOR FILING DATE: 2000-03-21	;	;	;
		NUMBER OF SEQ ID NOS: 10	;	;	;
		SOFTWARE: PatentIn version 3.0	;	;	;
		SEQ ID NO 4	;	;	;
		LENGTH: 616	;	;	;
		TYPE: PRT	;	;	;
		ORGANISM: Salmon Anaemia Virus	;	;	;
		US-10-049-086-4	;	;	;

Query Match	100.0%	Score 3097;	DB 2;	Length 616;	
Best Local Similarity	100.0%	Pred. No. 3 , e-309	;	;	;
Matches	616 , Conservative	Mismatches 0 ; Indels 0 ; Gaps 0 ;	;	;	;
Qy	1 MADKGNTYSPFDVNDTLLVVRSTATSGKIKISYRDRGTSLLQKAFAAGTEDBFWVLDQD 60	Db	1 MADKGNTYSPFDVNDTLLVVRSTATSGKIKISYRDRGTSLLQKAFAAGTEDBFWVLDQD 60		
Qy	1 MADKGNTYSPFDVNDTLLVVRSTATSGKIKISYRDRGTSLLQKAFAAGTEDBFWVLDQD 60	Db	1 MADKGNTYSPFDVNDTLLVVRSTATSGKIKISYRDRGTSLLQKAFAAGTEDBFWVLDQD 60		
Qy	61 VYDOKKTRKPLERKMKOMSTRVSGAAAIIERSVDPNSKEAAANIEMAGVDDBAGG 120	Db	61 VYDOKKTRKPLERKMKOMSTRVSGAAAIIERSVDPNSKEAAANIEMAGVDDBAGG 120		
Qy	121 SGLVDNRRNGKVGSMAATNLSLFGMVFALTTFSAILSBRGENSIWQNQAIIRILALA 180	Db	121 SGLVDNRRNGKVGSMAATNLSLFGMVFALTTFSAILSBRGENSIWQNQAIIRILALA 180		
Qy	181 DEDGRQTRGTSQYDMDYTKLNVTANGKVSKYQEVNLDKAFAFRQSRPKRSYRKQG 240	Db	181 DEDGRQTRGTSQYDMDYTKLNVTANGKVSKYQEVNLDKAFAFRQSRPKRSYRKQG 240		
Qy	241 GSKEATSSISNOCMALIMKSVLSDQLPAPGVKMRTRNGPNASTTLAEGANISPSKLRLH 300	Db	241 GSKEATSSISNOCMALIMKSVLSDQLPAPGVKMRTRNGPNASTTLAEGANISPSKLRLH 300		
Qy	241 GSKEATSSISNOCMALIMKSVLSDQLPAPGVKMRTRNGPNASTTLAEGANISPSKLRLH 300	Db	241 GSKEATSSISNOCMALIMKSVLSDQLPAPGVKMRTRNGPNASTTLAEGANISPSKLRLH 300		

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OM protein - protein search, using sw model 1

Run on: January 13, 2006, 09:27:06 ; Search time 65 Seconds (without alignments)

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main.*

1: /cmn2_6_ptodata/1/pubpba/us07_pubcomb.pep:
2: /cmn2_6_ptodata/1/pubpba/us08_pubcomb.pep:
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4: /cmn2_6_ptodata/1/pubpba/us10_pubcomb.pep:
5: /cmn2_6_ptodata/1/pubpba/us10_pubcomb.pep:
6: /cmn2_6_ptodata/1/pubpba/us11_pubcomb.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	3097	100.0	616	4	US-10-734-782-4 Sequence 4, Appli
2	3097	100.0	616	6	US-11-083-801-4 Sequence 4, Appli
3	3093	99.5	616	4	US-10-472-990-6 Sequence 6, Appli
4	128	4.1	1556	4	US-10-369-493-1796 Sequence 1796, Ap
5	126	4.1	957	4	US-10-607-631-12 Sequence 12, Appli
6	121	3.9	1377	4	US-10-450-763-52631 Sequence 52631, A
7	121.5	3.9	954	4	US-10-450-763-52631 Sequence 52631, A
8	121	3.9	2402	4	US-10-661-809-20 Sequence 47115, A
9	119	3.8	735	4	US-10-767-701-46665 Sequence 46665, A
10	119	3.8	872	4	US-10-632-585-7421 Sequence 7421, A
11	118.5	3.8	1483	4	US-10-282-122A-51483 Sequence 51483, A
12	117	3.8	1226	5	US-10-471-934-2 Sequence 2, Appli
13	117	3.8	1226	5	US-10-471-934-16 Sequence 16, Appli
14	116.5	3.8	1166	4	US-10-282-122A-51888 Sequence 51888, A
15	116.5	3.8	2042	4	US-10-192-584-6 Sequence 6, Appli
16	116	3.7	839	4	US-10-369-493-13153 Sequence 13153, A
17	116	3.7	1166	5	US-10-744-672-7 Sequence 7, Appli
18	116	3.7	1166	5	US-10-744-616-7 Sequence 7, Appli
19	116	3.7	1166	5	US-10-470-048B-152 Sequence 153, Appli
20	116	3.7	2516	4	US-10-437-963-162525 Sequence 162525, Appli
21	115.5	3.7	1191	4	US-10-282-122A-52048 Sequence 52048, A
22	115	3.7	1095	4	US-10-193-764-65 Sequence 65, Appli
23	115	3.7	1536	4	US-10-92-880-2 Sequence 2, Appli
24	115	3.7	1536	4	US-10-193-764-63 Sequence 63, Appli
25	115	3.7	1536	4	US-10-681-171-2 Sequence 2, Appli
26	114.5	3.7	1086	4	US-10-282-122A-74458 Sequence 74458, A
27	114.5	3.7	4560	5	US-10-398-200-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-734-782-4
; Sequence 4, Application US/10734782
; Publication No. US200401468601
; GENERAL INFORMATION:
; APPLICANT: Griffiths, Steven
; TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences Of
; TITLE OF INVENTION: Infectious Salmon Anaemia Virus And Their Uses As Vaccines
; FILE REFERENCE: H-323183
; CURRENT APPLICATION NUMBER: US/10/734-782
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/049, 086
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: PCT/GB00/02976
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: GB 0006674. 6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: GB 0005848. 7
; PRIOR FILING DATE: 2000-03-11
; PRIOR APPLICATION NUMBER: GB 9918588. 6
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Infectious salmon Anaemia Virus
US-10-734-782-4

Query Match 100.0% ; Score 3097; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 6.8e-270;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MADKGITYSFYDQNTLYVRRSTATSGKIKTSYREDGTSLLQKAFAGTEDFVWLDQD 60
2 1 MADKGITYSFYDQNTLYVRRSTATSGKIKTSYREDGTSLLQKAFAGTEDFVWLDQD 60
3 61 VYVDKLRKEBEKQKDMSTRVSQAVAAATERSVBDNFSEKAANJEMAGYDDBZAGG 120
4 1 MADKGITYSFYDQNTLYVRRSTATSGKIKTSYREDGTSLLQKAFAGTEDFVWLDQD 60
5 61 VYVDKLRKEBEKQKDMSTRVSQAVAAATERSVBDNFSEKAANJEMAGYDDBZAGG 120
6 1 SGLYDVKRKGKTSVNNAYNLSLFIGHYFPALETTFFSAILSEGEMSIWONGQATIRITALA 180
7 121 SGLYDVKRKGKTSVNNAYNLSLFIGHYFPALETTFFSAILSEGEMSIWONGQATIRITALA 180
8 121 SGLYDVKRKGKTSVNNAYNLSLFIGHYFPALETTFFSAILSEGEMSIWONGQATIRITALA 180

Copyright (c) 1993 - 2006 Compugen Ltd.	GenCore version 5.1.6	30	110	3.6	649	2	AP2866
OM protein - protein search, using sw model		31	110	3.6	670	2	C9763
Run on:	January 13, 2006, 09:27:05 ; Search time 20 Seconds (without alignments)	32	109.5	3.5	683	2	D83511
Title:	US-10-734-782-4	33	109.5	3.5	1220	2	S13057
Perfect score:	3097	34	109.5	3.5	2570	2	T17451
Sequence:	1 MADKGMYSFDVDRNTLIVR.....DMTPBIEFDDDEESEIDIDI 616	35	109.5	3.5	2660	2	E85822
Scoring table:	BLOSUM62	36	109.5	3.5	3488	2	T34418
Gapop:	10.0 , Gapext 0.5	37	109	3.5	470	2	Protein_C16A3.2 [i]
Searched:	283416 seqs, 96216763 residues	38	109	3.5	1810	2	E88481
Total number of hits satisfying chosen parameters:	283416	39	109	3.5	1819	2	Uncharacterized ph
Minimum DB seq length:	0	40	109	3.5	1926	2	DNA-binding nuclea
Maximum DB seq length:	2000000000	41	108.5	3.5	594	2	hypothetical prote
Post-processing:	Minimum Match 0%	42	108.5	3.5	1081	2	hypothetical prote
	Maximum Match 100%	43	108.5	3.5	1562	2	probable lipoprote
	Listing First 45 summaries:	44	108.5	3.5	3679	2	DNA repair and gen
		45	108	3.5	1335	2	repair
					565	2	DNA repair and gen
					565	2	repair
					H83996		
							ALIGMENTS
							RESULT 1
							S59393
							probable membrane protein YLR247C - Yeast (Saccharomyces cerevisiae)
							N;Alternate names: hypothetical protein L9672.14
							C;Species: Saccharomyces cerevisiae
							C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
							C;Accession: S59393
							R;Johnson, D.
							Submitted to the EMBL Data Library, February 1995.
							A;Description: The sequence of <i>S. cerevisiae</i> cosmid 9672.
							A;Reference number: S59393
							A;Molecule type: DNA
							A;Cross-references: SGD:S0004237
							A;Map position: 1-1556 <JOH>
							A;Cross-references: UNIPROT:Q06554; UNIPARC:UP10000069EBB; EMBL:U20865; NID:g662330; PID:962330
							A;Experimental source: strain S288C (AB972)
							C;Genetics:
							A;Gene: MIPS:YLR247C
							A;Cross-references: SGD:S0004237
							A;Map position: 1-1556
							C;Keywords: transmembrane protein
							P;1225-1282/Domain: RING finger homology <RRN>
							F;1236-1252/Domain: transmembrane #status predicted <TMM>
							Query Match 4.1%; Score 128; DB 2; Length 1556;
							Best Local Similarity 19.1%; Pred. No. 2-6;
							Matches 125; Conservative 111; Mismatches 194; Gaps 34;
							Qy 24. ATKGKIKSYREDRGTSILQKAFAAGTEDPFWVHL---DQDVYDKCIRKPLERHKMD 79
							Db 778 ALSSPIKC--RDDIMIHIQK--FNVEDPDFKSINLSBDEDEBDRFGS--KETSSGDS 831
							Qy 80 STR-VSGAVAAAERSVEDDNFSKRAANIEAMGVDDBEAGGSILVDNRKNG--YVSN 135
							Db 832 SDREINGA-----KHDHNND-----GMLSNHLLKKCKRARMNN 865
							Qy 136 MAANLISLIFGMVPPALT-----PSAILSEGEM-SIWQN----ND 221
							Db 866 LLHDGYFFGSDVYNLGRKLEBADKHKEKTEVVYSDVFPKNELEBEEPNLQBEN 925
							Qy 170 --GQAIIIRLLALADBGKRQTRTGQRYDMA--DVTKLAVVTTANGKVQEVNL--ND 222
							Db 926 YANABILRSILSS-----ARKVDMTIRKARTKAPMTSNIPRLINTBDPHND 976
							Qy 977 YSSNLAVSRCEFCISLKLLEGLNCTKNFNLDELLLIYEPVTEREDDDSTNCKIGNE 1036
							Db 222 LKAAPRQSPRKRS-----DYGKQGSKA 244
							Qy 245 TESSISNQ-----CMALIMK--SVLSDAQLPAGYTKMRTNGFNASYTTLAEGANI 293
							Db 1037 YSSNISDSQDKIFSLLGCLLILQRDNLTSES---EVKIPK-----HVPCESSI 1083

Result No.	Score	Query	Match	Length	DB	ID	Description
1	3097	100.0	616	2	Q91BR3_9ORTO		Q91BR3_9ORTO PRELIMINARY;
2	3083	99.5	616	2	08V3T7_9ORTO		AC Q91BR3/_
3	3067	99.0	616	2	06YN41_9ORTO		DT 01-DBC-2001 (TREMBLrel. 19, Created)
4	3029	97.8	616	2	098VU1_9ORTO		DT 01-DBC-2001 (TREMBLrel. 19, Last sequence update)
5	152	4.9	1758	2	09JMS5_ECOLI		DT 01-BAR-2004 (TREMBLrel. 26, Last annotation update)
6	143.5	4.6	6084	2	087TID8_VIBPZA		DB Putative nucleoprotein.
7	131.5	4.2	2089	2	092K98_RHIME		OS Infectious salmon anemia virus.
8	130.5	4.2	794	2	07YY86_CRYPV		OC ssRNA negative-strand viruses; Orthomyxoviridae; Isavirus.
9	129	4.2	1023	2	093T53_STRPY		RN [1] NCBI_TaxID=55387;
10	128	4.1	6077	2	091L85_WSAYST		RP NUCLEOTIDE SEQUENCE.
11	128	4.1	1556	2	060554_YBAST		RX MEDLINEB=2134212; PubMed=11450947; DOI=10.1023/A:1011110105819;
12	127	4.1	566	2	074S05_YERPS		RX Ritchie R.J., Heppell J., Cook M.B., Jones S., Griffiths S.G.;
13	127	4.1	566	2	0BCZXT_YERPS		RX "Identification and characterization of segments 3 and 4 of the ISAV genome.", Virus Genes 22:289-297 (2001).
14	126	4.1	764	2	04HG87_CAMCO		RL EMBJB=AP206549; AAC97306.1; mENA.
15	126	4.1	957	2	0000SO_MICHY		DR InterPro; IPR006089; Acyl-CoA_dh.
16	126	4.1	6077	2	08QB77_WSSV		KW PROSITE; PS00073; ACYL_COA_DH_2; UNKNOWN_1.
17	126	4.1	6077	2	08VAP1_WSSV		KW Viral nucleoprotein.
18	125	4.0	1175	2	047955_HARDU		SQ SEQNCNRRKKGTSNMAATNLSPIGMVPALITPPSALLSEGNSIWONGQAIIIRILALA 120
19	125	4.0	1175	2	07VLT6_HAEDU		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
20	124.5	4.0	1087	2	08W1Y3_ARATH		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
21	124.5	4.0	3165	2	08RDQ9_FUSNN		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
22	123	4.0	892	2	06BZAJ_DEBHA		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
23	123	4.0	1314	2	070251_ANOGA		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
24	122	3.9	1203	1	SMC2_XENLA		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
25	121.5	3.9	799	2	04PGW1_USTWA		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
26	121.5	3.9	1377	2	04PB1_BORLU		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
27	121.5	3.9	3620	2	05XW66_BARVI		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
28	121	3.9	862	2	0615W4_CABER		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
29	121	3.9	2402	2	09AER7_STAPP		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
30	121	3.9	2402	2	05HCKF4_STABQ		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120
31	120.5	3.9	959	2	Q8S950_TOBAC		61 VYDVKRKIRPLFEERKDKMSTRYSGAVAAAIERSVEFDFNSKEAANIMAGYDBEAGG 120

ALIGNMENTS

RESULT 1							
US-11-083-800-4							
Sequence 4, Application US-11083800							
Publication No. US20050261227A1							
GENERAL INFORMATION:							
APPLICANT: Griffiths, Steven							
APPLICANT: Ritchie, Rachael Jane							
TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences Of							
TITLE OF INVENTION: Infectious Salmon Anaemia Virus And Their Uses As Vaccines							
FILE REFERENCE: H-3223LB							
CURRENT APPLICATION NUMBER: US-11/083-800							
CURRENT FILING DATE: 2005-03-18							
PRIOR APPLICATION NUMBER: US 10/049,086							
PRIOR FILING DATE: 2002-02-06							
PRIOR APPLICATION NUMBER: PCT/GB00/02976							
PRIOR FILING DATE: 2000-08-07							
PRIOR APPLICATION NUMBER: GB 0006674.6							
PRIOR FILING DATE: 2000-03-21							
PRIOR APPLICATION NUMBER: GB 0005848.7							
PRIOR FILING DATE: 2000-03-11							
PRIOR APPLICATION NUMBER: GB 9918588.6							
PRIOR FILING DATE: 1999-08-07							
NUMBER OF SEQ ID NOS: 10							
SOFTWARE: FastSEQ for Windows Version 4.0							
SEQ ID NO 4							
TYPE: PRT							
ORGANISM: Infectious Salmon Anaemia Virus							
US-11-083-800-4							
Query	Score	Match	Length	DB	ID	Description	
result	No:						
1	3097	100.0	616	7	US-11-083-800-4	Sequence 4, Appli	
2	116.5	3.8	1086	7	US-11-052-554A-380	Sequence 86, Appli	
3	113.5	3.7	2053	7	US-11-013-759-9	Sequence 9, Appli	
4	112.5	3.6	1572	6	US-10-793-626-2906	Sequence 2906, Appli	
5	111	3.6	1992	7	US-11-013-759-3	Sequence 3, Appli	
6	111	3.6	1992	7	US-11-013-759-3	Sequence 13, Appli	
7	111	3.6	2047	7	US-11-013-759-4	Sequence 4, Appli	
8	111	3.6	2047	7	US-11-013-759-7	Sequence 7, Appli	
9	108.5	3.5	1300	7	US-11-052-554A-125	Sequence 125, Appli	
10	105	3.4	2314	7	US-11-013-759-11	Sequence 11, Appli	
11	103	3.3	5291	7	US-11-052-554A-281	Sequence 281, Appli	
12	102	3.3	1916	7	US-11-069-834-54	Sequence 52, Appli	
13	102	3.3	1916	7	US-11-069-834-54	Sequence 54, Appli	
14	101	3.3	446	7	US-11-196-475-54	Sequence 154, Appli	
15	101	3.3	531	7	US-11-069-834-54	Sequence 4, Appli	
16	101	3.3	2233	6	US-10-873-528-12	Sequence 2, Appli	
17	100.5	3.2	522	6	US-10-793-626-56	Sequence 456, Appli	
18	100.5	3.2	522	6	US-10-793-626-042	Sequence 2042, Appli	
19	100	3.2	930	6	US-10-821-234-188	Sequence 1188, Appli	
20	99.5	3.2	453	7	US-11-196-475-52	Sequence 152, Appli	
21	99.5	3.2	1970	6	US-10-811-234-1641	Sequence 1641, Appli	
22	99.5	3.2	2902	7	US-11-052-554A-91	Sequence 91, Appli	
23	99.5	3.2	3256	7	US-11-124-368A-104	Sequence 304, Appli	
24	98	3.2	424	6	US-10-485-517-264	Sequence 264, Appli	
25	98	3.2	424	6	US-10-485-517-264	Sequence 181, DEDGKRQTRGGVDRVDAVTGKVYVNTANGKTYOEVNINDLKAFTQRQPKRDKYKQ	